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PR 04-AUG-1997; 97US-0054642.

PA (CAMEB-) CAMEBIA BIOSYSTEMS LLC.
PI Bowtell D, Killian A;

DR WPI; 1999-106060/09.
DR P-PSDB; AAX00627.

XX New isolated vertebrate telomerase genes - used to develop products
XX for treating cancers or for organ regeneration, nerve cell or brain
XX cell growth following injury or bone marrow transplantation

PT Claim 3; Fig 1; 134pp; English.
XX This sequence encodes the human telomerase of the invention. Primers that
XX amplify the telomerase coding sequence can be used in a method for
XX diagnosing cancer in a patient. The telomerase can be used for detection,
XX used to treat cancers such as melanomas, other skin cancers,
XX neuroblastomas, breast carcinomas, colon carcinomas, leukemias,
XX lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
XX growths. Enhancers of telomerase may be used to stimulate stem cell
XX proliferation and differentiation (expansion of haematopoietic stem cells
XX in wound healing, hair growth, treatment of disease such as Wilms
XX tumour, organ regeneration or differentiation after injury or diseases,
XX nerve cell or brain cell growth following injury.

Sequence 3964 BP; 661 A; 1337 C; 1257 G; 709 T; 0 other.

alignment_scores:
Quality: 5866.00 Length: 1132
Ratio: 5.247 Gaps: 1
Percent Similarity: 98.763 Percent Identity: 98.763

alignment_block:
US-09-502-424-46 x AAX18254

Align seg 1/1 to: AAX18254 from: 1 to: 3964

1 MetProArgAlaProArgCysArgAlaValAlaSerLeuLeuArgSerH1 17
1 AAGCCGCGCGCTCCCGCTGCGAGCGCGCTCCCTGCTGCGCAGCA 50
17 sThrArgGluValLeuProLeuAlaThrPheValAlaArgArgLeuGlyProG 34
51 CTACCGGAGGCTGCTGCGCTGCGCAGCTTCTGCGCGCGCTGCGGCGCC 100.
34 lnglyTPArgLeuValAlaGlnArgGlyAspProAlaAlaPheArgAlaLeu 50
101 AGGCGCTGCGCGCTGCTGCGCAGCGCGGAGCGCGCGCTTTCGCGCGCTG 150
51 ValAlaGlnCysLeuValCysValProTirAspAlaArgProProProAl 67
151 GtGtGCGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 200
67 aAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAlaArgV 84
201 CCCCCCGCTTCCCGCGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 250
84 alLeuGlnArgLeuCysGlnArgGlyAlaAlaLysAsnValLeuAlaPheGly 100
251 TGCTGCAAGAGGCTGCTGCGAGCGCGCGCAAGACCTGCTGCTGCTGCG 300
101 PheAlaLeuLeuAspGlyAlaArgGlyLysProProGluAlaPheThrH 117
301 TTCGCGTGTGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCTTACAC 350
117 rSerValArgSerTyrLeuProAsnThrValThrAspAlaLeuArgGlys 134

351 CAGCGTGGCAGCTACCTGCTCCCAACAGCGGTGACCGACGACCTCGGGGA 400
134 erGlyAlaThrPglLeuLeuArgValAlaLysAspValLeuVal 150
401 GCGGCGCTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 450
151 HisLeuLeuAlaArgCysAlaLeuPheValLeuValAlaProSerCysAl 167
451 CACTGCTGCGCAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 500
167 aTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThrGlnA 184
501 CTACAGAGTGTGGGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 550
184 laArgProProProHAlaSerLysProArgArgArgGlyCysGlu 200
551 CCGGCG 600
201 ArgAlaThrAsnHisSerValArgGluAlaGlyValProLeuGlyLeuPr 217
601 CCGGCGCTGGACCATAGCTCAGGAGCGCGCGCGCGCGCGCGCGCG 650
217 oAlaProGlyAlaArgArgArgGlyLysSerAlaSerArgSerLeuProL 234
651 AGCCCG 700
234 euProLysArgProArgArgGlyAlaAlaProGluProGluArgThrPro 250
701 TGCCCAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 750
251 ValGlyGlnGlySerThrAlaHisProGlyArgThrArgGlyProSerAs 267
751 GTTGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 800
267 ParGlyPheCysValValSerProAlaArgProAlaGlnGluAlaThrS 284
801 CCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 850
284 erLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
851 CTTTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTr 317
901 CGCCAGCACACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 950
317 PASPTThrProCysProProValTyrAlaGlnThrLysHisPheLeuTyrS 334
951 GGAACCGCTTGTCCCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTG 1000
334 erSerGlyAspLysGlnGlnLeuArgProSerPheLeuLeuSerSerLeu 350
1001 CCTCAGCGCAGCAAGAGACCTGCGCGCTCCTTCTCCTACGAGCTCTG 1050
351 ArgProSerLeuThrGlyAlaArgArgLeuValGluThrLlePheLeuG 367
1051 AGGCCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1100
367 ySerArgProProMetProGlyThrProArgArgLeuProArgLeuProG 384
1101 TTCAGGCGCTGGATGCCAGGAGCTCCCGCAGGTGCGCGCGCTGCGCC 1150
384 lnaArgTyrTrpGlnMetArgProLeuPheLeuGlnLeuGlnLysAsnHis 400
1151 AGCGCTACTGGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4200
401 AlagLncysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAl 417
1201 GCGCAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1250
417 aAlaValThrProAlaAlaGlyValCysAlaArgGluLysProGlnLys 434

1251 TCGGCTCACCCGACGCGGCTGTCTGTCCCGGAGAGAGCCCGAGGCT 1300
434 erValAlaAlaProGluGluGluAspThrAspProArgArgValGln 450
1301 CTGTGGCGGCGCCGAGGAGGAGACACAGACCCCGCTGCTGTGTCAG 1350
451 LeuLeuArgGlnHisSerProTyrGlnValTyrGlyPheValArgAl 467
1351 CTGTCTCCGCGACACAGAGCCCTGTGAGGTGTACGGCTGTGCGGCG 1400
467 ACysLeuArgArgValProProGlyLeuTyrPglYserArgHisAsn 484
1401 CTGCTGGCGCGGCTGTGCTCCCGAGGCTGTGGGCTCCAGGCGACAG 1450
484 LuArgArgPheLeuArgAsnTyrLysPheLeuSerLeuGlyLysHis 500
1451 AACCGCGCTCTCCAGAGACACAGAGATTGATCTCTCCGTGGGAGAG 1500
501 AlaLysLeuSerLeuGlnGluLeuThrTyrPlysMetSerValArgAsp 517
1501 GCCAAGCTCTGCTGACAGAGCTGACGGAAGATGAGCGTGGGAGCTG 1550
517 AlaTyrLeuArgArgSerProGlyValGlyCysValProAlaAlaGlu 534
1551 CGCTTGGCTGCGAGAGGCCAGAGGCTGTGCTGTCCGCGCGAGAGC 1600
534 LsArgLeuArgGluGluLeuAlaLysPheLeuHisTyrLeuMetSer 550
1601 ACCGTCGCGGAGAGATCTGCGCAAGTTCCTGCACTGGCTGTAGAT 1650
551 ValTyrValAlaGluLeuLeuArgSerPhePheTyrValThrGluThr 567
1651 GTGAGCTCTCGAGCTGCTCGAGGTCTTCTTTATGTCAGAGAGACAC 1700
567 rPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTyrSerLys 584
1701 GTTTCAAAAGACAGGCTCTTCTTCTACCGAGAGAGTGTGGAGCAAG 1750
584 euGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArg 600
1751 TGCAGAGCATGTGAATCAGACAGACACTTGAAGAGGTGACAGCTCG 1800
601 LeuSerGlnAlaGluValArgGlnHisArgGluAlaArgProAlaLeu 617
1801 CTGTGGAGAGCAGAGGTCAAGGACATCGGGAAGCCAGGCGCGCTGT 1850
617 uThrSerArgLeuArgPheIleProLysProAspGlyLeuArgProIle 634
1851 GACGTCCAGACTCCGCTTCATCCCAAGCTGACGGGCTCGGCGGATG 1900
634 AlaMetLysPyrValValGlyAlaArgThrPheArgArgGlyLysArg 650
1901 TGACATGAGCTACGTCTGTGGAGCCAGAACCTTCGCGAGAAAGAG 1950
651 AlaGluArgLeuThrSerArgValLysAlaLeuPheSerValLeuAsn 667
1951 GCCGAGCGCTCACTCGAGGCTGAAGGACACTTGAAGGCTGTCAACTA 2000
667 rGluArgAlaArgArgProGlyLeuLeuGlyLysSerValLeuGlyLeu 684
2001 CGAGGCGGCGGCGCGCGCTGTGCGGCTGTGCTGTGCTGTGCGGCTG 2050
684 spAspIleHisArgAlaTyrPheThrPheValLeuArgValArgAlaGln 700
2051 ACGATATCCACAGGCGCTGCGGCACTTCGTGCTGTGCTGTGCGGCG 2100
701 AspProProProGluLeuTyrPheValLys..... 710
2101 GATCGCGCGCTGTGAGCTGTACTTGTCAAGGAGATGTGAGCGGCGCTA 2150
711AspArgLeuThrGluValIleAlaSerIleIle 722
2151 CGACACCATCCCGGAGGACAGGCTCAGGAGGTCTATCGCCAGACATCA 2200
722 ysProGlnAsnThrTyrCysValArgArgTyrAlaValAlaGlnLysAla 738
2201 AACCCAGACACAGTACGTGCGGTGCTGTGTATGCGGTGTCCAGAGGCG 2250
739 AlaHisGlnHisValArgLysAlaPheLysSerHisValSerThrLeu 755
2251 GCCCATGGGACAGTCCCGCAGGCGCTTCAAGACCGACGTCTTACTGAC 2300
755 rAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnLysHis 772
2301 AGACCTCCAGGCTGATCAGACAGATTGCTGCTCAGCTTCACTGAGAG 2350
772 erProLeuArgAspAlaValAlaIleGluGlnSerSerSerLeuAsnGlu 788
2351 GCCCGGAGGAGGATGCGTGTGATTCAGACAGAGCTCTCTGATATGAG 2400
789 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAl 805
2401 GCCAGAGTGGCTCTTGTGAGAGTCTTCTTCAAGCTTCACTGCTCCAGC 2450
805 aValArgIleArgGlyLysSerTyrValGlnCysGlnGlyIleProGln 822
2451 CGTGGCATCAGGAGGCAAGTCTACGTCAGTCCAGTCCAGGAGATCCCG 2500
822 LysrIleLeuSerThrLeuLeuLysSerLeuLysCysTyrGlyAspMetGlu 838
2501 GCTCCATCTCTCCAGGCTCTCTGACAGCTGTGCTTACAGGCGACATGAG 2550
839 AsnLysLeuPheAlaGlyIleArgArgAspGlyLeuLeuLeuArgLeu 855
2551 AACCACTCTTGTGGGAGATTCGCGGAGCGGCGGTGCTCTGCGTTGGT 2600
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872 euArgThrLeuValArgGlyValProGluTyrGlyCysValAlaAsnLeu 888
2651 TCAGACCTCTGTCGAGGTGTCCTGATGATGCGCGGTGCGGACTTG 2700
889 ArgLysThrValAlaAsnPheProValGluAspGlyAlaLeuGlyLys 905
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955 YAsnMetLysArgLysLeuPheGlyValLeuArgPheLysCysHis 972
2901 GAGGACATCGTGCAGAACTCTTGGGCTTTCGCGCTGAGAGTGTACA 2950
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989 IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLe 1005
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